RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/588,140 _____
Source: _____ JFWO _____
Date Processed by STIC: _____ 08/10/2006 _____

ENTERED

RAW SEQUENCE LISTING   DATE: 08/10/2006
PATENT APPLICATION: US/10/588,140   TIME: 10:59:47

Input Set : A:\44352-0010-00-US sequence listing(pct 05 234).txt
Output Set: N:\CRF4\08102006\J588140.raw

```
      3 <110> APPLICANT: Lifenza Co., Ltd.
      5 <120> TITLE OF INVENTION: PROTEIN WITH ACTIVITY OF HYDROLYZING DEXTRAN, STARCH, MUTAN,
      6       INULIN AND LEVANN, GENE ENCODING THE SAME, CELL EXPRESSING THE
      7       SAME, AND PRODUCTION METHOD THEREOF
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/588,140
C-->  9 <141> CURRENT FILING DATE: 2006-07-31
W-->  0 <130> FILE REFERENCE:
      9 <150> PRIOR APPLICATION NUMBER: KR2004-0006185
     10 <151> PRIOR FILING DATE: 2004-01-30
     12 <160> NUMBER OF SEQ ID NOS: 4
     14 <170> SOFTWARE: KopatentIn 1.71
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 608
     18 <212> TYPE: PRT
     19 <213> ORGANISM: Artificial Sequence
     21 <220> FEATURE:
     22 <223> OTHER INFORMATION: S. cerevisiae/pYES2-LSD1
     25 <400> SEQUENCE: 1
     26 Met Thr Leu Ile Tyr Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile
     27  1           5                   10                  15
     29 Thr Arg Ile Val Leu Val Asn Ile Leu Leu Ala Thr Leu Val Leu Gly
     30              20                  25                  30
     32 Ala Ala Val Leu Pro Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu
     33          35                  40                  45
     35 Cys Thr Trp Trp His Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val
     36      50                  55                  60
     38 Gln Ala Gly Asn Val Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser
     39  65                  70                  75                  80
     41 Leu Ala Asp Arg Asn Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile
     42              85                  90 ·                95
     44 Pro Arg Asn Gly Asn Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn
     45              100                 105                 110
     47 Ser Asn Thr Leu Asn Ser Ser Ile Asp Asp Gly Ile Ser Ile Glu Pro
     48          115                 120                 125
     50 Ser Leu Gly Ile Asn Met Ala Trp Ser Gln Phe Glu Tyr Arg Arg Asp
     51      130                 135                 140
     53 Val Asp Ile Lys Ile Thr Thr Ile Asp Gly Ser Ile Leu Asp Gly Pro
     54 145                 150                 155                 160
     56 Leu Asp Ile Val Ile Arg Pro Thr Ser Val Lys Tyr Ser Val Lys Arg
     57              165                 170                 175
     59 Cys Val Gly Gly Ile Ile Ile Arg Val Pro Tyr Asp Pro Asn Gly Arg
     60              180                 185                 190
     62 Lys Phe Ser Val Glu Leu Lys Ser Asp Leu Tyr Ser Tyr Leu Ser Asp
```

```
63          195               200               205
65 Gly Ser Gln Tyr Val Thr Ser Gly Gly Ser Val Val Gly Val Glu Pro
66      210               215               220
68 Lys Asn Ala Leu Val Ile Phe Ala Ser Pro Phe Leu Pro Arg Asp Met
69 225               230               235               240
71 Val Pro His Met Thr Pro His Asp Thr Gln Thr Met Lys Pro Gly Pro
72              245               250               255
74 Ile Asn Asn Gly Asp Trp Gly Ser Lys Pro Ile Leu Tyr Phe Pro Pro
75          260               265               270
77 Gly Val Tyr Trp Met Asn Glu Asp Thr Ser Gly Asn Pro Gly Lys Leu
78      275               280               285
80 Gly Ser Asn His Met Arg Leu Asp Pro Asn Thr Tyr Trp Val His Leu
81      290               295               300
83 Ala Pro Gly Ala Tyr Val Lys Gly Ala Ile Glu Tyr Phe Thr Lys Gln
84 305               310               315               320
86 Asn Phe Tyr Ala Thr Gly His Gly Val Leu Ser Gly Glu Asn Tyr Val
87              325               330               335
89 Tyr Gln Ala Asn Ala Ala Asp Asn Tyr Tyr Ala Val Lys Ser Asp Gly
90          340               345               350
92 Thr Ser Leu Arg Met Trp Trp His Asn Asn Leu Gly Gly Gly Gln Thr
93          355               360               365
95 Trp Phe Cys Met Gly Pro Thr Ile Asn Ala Pro Pro Phe Asn Thr Met
96      370               375               380
98 Asp Phe Asn Gly Asn Ser Asn Ile Ser Ser Arg Ile Ser Asp Tyr Lys
99 385               390               395               400
101 Gln Val Gly Ala Tyr Phe Phe Gln Thr Asp Gly Pro Glu Ile Tyr Glu
102              405               410               415
104 Asp Ser Val Val His Asp Val Phe Trp His Val Asn Asp Asp Ala Ile
105          420               425               430
107 Lys Thr Tyr Tyr Ser Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys
108          435               440               445
110 Cys His Asn Asp Pro Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu
111      450               455               460
113 Thr Gly Ile Ser Ile Asp Asn Leu His Val Ile His Thr Arg Tyr Phe
114 465               470               475               480
116 Lys Ser Glu Thr Val Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe
117              485               490               495
119 Tyr Ala Ser Gly Met Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr
120          500               505               510
122 Ile Ser Asn Val Val Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile
123          515               520               525
125 Thr Pro Leu Gln Ser Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe
126      530               535               540
128 Pro Asp Gly Leu Gln Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile
129 545               550               555               560
131 Pro Ala Ala Ser Gly Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr
132          565               570               575
134 Val Lys Gly Gln Lys Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu
135          580               585               590
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137 Gly Gln Phe Asp Ile Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn
138        595                   600                   605
143 <210> SEQ ID NO: 2
144 <211> LENGTH: 2052
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: S. cerevisiae/pYLSD1
152 <400> SEQUENCE: 2
153 tgggtgtgtc ccttgctctg ccaacgttgt tgattgtttt catgacatta atctacgtgc      60
155 cttcaatatt tacaatggtc ccctcaatca cacggattgt actggttaac attctgttgg     120
157 cgacgttggt tttgggagct gcagtccttc cacgagacaa cagaactgtt tgcgggagtc     180
159 aactctgcac atggtggcac gactccggcg agataaacac cggtactcct gtacaggcag     240
161 gaaacgttcg acaatcccga aagtactctg tccatgtgag cctggcagac cgtaaccaat     300
163 tctacgactc tttcgtatat gaatcgatac ctaggaacgg caatggcaga atttattctc     360
165 ccaccgaccc acctaacagc aatacattga atagtagcat tgacgacggt atatcaatcg     420
167 aaccatctct cggcatcaac atggcttggt cccagttcga atatagacga gatgtcgaca     480
169 ttaagattac tacaatcgat ggctcaatat tggatggccc tttggacatt gttattcggc     540
171 cgacttctgt taagtactca gtcaaaagat gtgtgggtgg tatcattatt agagtccctt     600
173 atgatcccaa tggtcgaaaa ttctctgttg agttaaagag tgacctttac agttacctct     660
175 ccgacggttc gcaatatgtg acctctggag ggagcgtggt tggtgtggag ccaaaaaatg     720
177 ccctggtgat ctttgccagc cctttcttgc cacgggatat ggttcctcat atgacaccac     780
179 acgacaccca gacaatgaag ccgggcccaa tcaataatgg ggactggggt tcaaagccta     840
181 tactctactt cccgcctggc gtatactgga tgaacgagga tacctctggt aaccccggga     900
183 agctcggctc aaatcatatg cggctggatc ccaataccta ctgggtccat ctagccccag     960
185 gagcctatgt gaaaggagcc attgagtatt tcacgaagca aaatttctat gcaacgggtc    1020
187 atggcgttct ctcaggtgag aactatgttt atcaggccaa tgcagctgat aactactatg    1080
189 ccgtcaagag tgatggcaca agcttgagaa tgtggtggca caacaacctt ggaggcggtc    1140
191 aaacatggtt ttgcatgggg cccaccatta atgcaccgcc gtttaatacg atggacttca    1200
193 acggaaactc taatatttcc agccggatta gtgactataa gcaggttggc gcttattttt    1260
195 tccaaacaga cggaccggag atctacgagg acagtgttgt ccatgacgtc ttctggcatg    1320
197 ttaatgatga tgccatcaag acatattatt ccggagcttc aatttcacga gcaaccatct    1380
199 ggaagtgtca caatgacccg atcatacaga tgggctggac gtcacgaaat ctcaccggaa    1440
201 tcagcattga taacctgcac gtcatccaca cgagatattt caaatctgaa acagtggttc    1500
203 cttcagcaat cattggagcg tctccattct acgcaagtgg aatgactgtt gatcccagcg    1560
205 agtccatcag catgaccatc tctaacgtgg tgtgtgaggg tctatgcccc tcactgttcc    1620
207 gtatcactcc gcttcagagc tacaacaacc ttgttgtcaa gaacgtggcc tttcccgatg    1680
209 gactgcagac aaatccaatc ggaataggag agagcattat accagcagct tccggctgta    1740
211 caatggactt ggaaatcaca aactggaccg tcaaggaca  aaaagtcacc atgcaaaact    1800
213 ttcagtccgg gtcacttggc cagttcgata tcgatggttc atactggggt caatggtcca    1860
215 taaactaaag ctattcccat tcacctgagt attttcgtgg gttcaatgag ttcttgttac    1920
217 tgatggggcc cttgctagtg gtaaaagtag agggacttgt cctcgccggg cgccaaggaa    1980
219 gttcatgtct tctagttgaa tagtatttgt ttcttctctc tcgttaaaaa aaaaaaaaa    2040
221 aaaaaaaaaa aa                                                        2052
224 <210> SEQ ID NO: 3
225 <211> LENGTH: 18
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 08/10/2006
.PATENT APPLICATION: US/10/588,140   TIME: 10:59:47

Input Set : **A:\44352-0010-00-US sequence listing(pct 05 234).txt**
Output Set: **N:\CRF4\08102006\J588140.raw**

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230 <223> OTHER INFORMATION: L. starkeyi DX-F primer(sense)
233 <400> SEQUENCE: 3
234 gtcccttgag ctcccaac                                            18
237 <210> SEQ ID NO: 4
238 <211> LENGTH: 23
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: L. starkeyi DX-R primer(antisense)
246 <400> SEQUENCE: 4
247 tcaactagaa ttcatgaact tcc                                      23
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VERIFICATION SUMMARY   DATE: 08/10/2006
PATENT APPLICATION: **US/10/588,140**   TIME: 10:59:48

Input Set : **A:\44352-0010-00-US sequence listing(pct 05 234).txt**
Output Set: **N:\CRF4\08102006\J588140.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE